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RAW SEQUENCE LISTING DATE: 05/31/2002
PATENT APPLICATION: PCT/US02/14570 TIME: 09:05:49

Input Set : A:\3198-WO.txt
Output Set: N:\CRF3\05312002\PU14570.raw

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      3 <110> APPLICANT: IMMUNEX CORPORATION
      4       Derry, Jonathan M. J.
      5       Fanslow III, William
      6       Dougall, William C.
      8 <120> TITLE OF INVENTION: SCREENING ASSAYS FOR AGONISTS OR ANTAGONISTS OF CD40
SIGNALING
     10 <130> FILE REFERENCE: 3198-WO
C--> 12 <140> CURRENT APPLICATION NUMBER: PCT/US02/14570
     13 <141> CURRENT FILING DATE: 2002-05-07
     15 <150> PRIOR APPLICATION NUMBER: 09/851,673
     16 <151> PRIOR FILING DATE: 2001-05-08
     18 <160> NUMBER OF SEQ ID NOS: 4
     20 <170> SOFTWARE: PatentIn version 3.1
     22 <210> SEQ ID NO: 1
     23 <211> LENGTH: 1994
     24 <212> TYPE: DNA
     25 <213> ORGANISM: Homo sapiens
     27 <220> FEATURE:
     28 <221> NAME/KEY: CDS
     29 <222> LOCATION: (149)..(1405)
     30 <223> OTHER INFORMATION:
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     36 ccgcagacta tcaatcccag tctcttcccc tcactccctg tgaagctctc cagcatcatc     120
     38 gaggtcccat cagcccttgc cctgttgg atg aat agg cac ctc tgg aag agc        172
     39                                Met Asn Arg His Leu Trp Lys Ser
     40                                1               5
     42 caa ctg tgt gag atg gtg cag ccc agt ggt ggc ccg gca gca gat cag      220
     43 Gln Leu Cys Glu Met Val Gln Pro Ser Gly Gly Pro Ala Ala Asp Gln
     44     10                  15                  20
     46 gac gta ctg ggc gaa gag tct cct ctg ggg aag cca gcc atg ctg cac      268
     47 Asp Val Leu Gly Glu Glu Ser Pro Leu Gly Lys Pro Ala Met Leu His
     48 25                  30                  35                  40
     50 ctg cct tca gaa cag ggc gct cct gag acc ctc cag cgc tgc ctg gag      316
     51 Leu Pro Ser Glu Gln Gly Ala Pro Glu Thr Leu Gln Arg Cys Leu Glu
     52                 45                  50                  55
     54 gag aat caa gag ctc cga gat gcc atc cgg cag agc aac cag att ctg      364
     55 Glu Asn Gln Glu Leu Arg Asp Ala Ile Arg Gln Ser Asn Gln Ile Leu
     56             60                  65                  70
     58 cgg gag cgc tgc gag gag ctt ctg cat ttc caa gcc agc cag agg gag      412
     59 Arg Glu Arg Cys Glu Glu Leu Leu His Phe Gln Ala Ser Gln Arg Glu
     60         75                  80                  85
     62 gag aag gag ttc ctc atg tgc aag ttc cag gag gcc agg aaa ctg gtg      460
     63 Glu Lys Glu Phe Leu Met Cys Lys Phe Gln Glu Ala Arg Lys Leu Val
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66  gag aga ctc ggc ctg gag aag ctc gat ctg aag agg cag aag gag cag      508
67  Glu Arg Leu Gly Leu Glu Lys Leu Asp Leu Lys Arg Gln Lys Glu Gln
68  105                 110                 115                 120
70  gct ctg cgg gag gtg gag cac ctg aag aga tgc cag cag cag atg gct      556
71  Ala Leu Arg Glu Val Glu His Leu Lys Arg Cys Gln Gln Gln Met Ala
72                  125                 130                 135
74  gag gac aag gcc tct gtg aaa gcc cag gtg acg tcc ttg ctc ggg gag      604
75  Glu Asp Lys Ala Ser Val Lys Ala Gln Val Thr Ser Leu Leu Gly Glu
76              140                 145                 150
78  ctg cag gag agc cag agt cgc ttg gag gct gcc act aag gaa tgc cag      652
79  Leu Gln Glu Ser Gln Ser Arg Leu Glu Ala Ala Thr Lys Glu Cys Gln
80          155                 160                 165
82  gct ctg gag ggt cgg gcc cgg gcg gcc agc gag cag gcg cgg cag ctg      700
83  Ala Leu Glu Gly Arg Ala Arg Ala Ala Ser Glu Gln Ala Arg Gln Leu
84      170                 175                 180
86  gag agt gag cgc gag gcg ctg cag cag cag cac agc gtg cag gtg gac      748
87  Glu Ser Glu Arg Glu Ala Leu Gln Gln Gln His Ser Val Gln Val Asp
88  185                 190                 195                 200
90  cag ctg cgc atg cag ggc cag agc gtg gag gcc gcg ctc cgc atg gag      796
91  Gln Leu Arg Met Gln Gly Gln Ser Val Glu Ala Ala Leu Arg Met Glu
92                  205                 210                 215
94  cgc cag gcc gcc tcg gag gag aag agg aag ctg gcc cag ttg cag gtg      844
95  Arg Gln Ala Ala Ser Glu Glu Lys Arg Lys Leu Ala Gln Leu Gln Val
96              220                 225                 230
98  gcc tat cac cag ctc ttc caa gaa tac gac aac cac atc aag agc agc      892
99  Ala Tyr His Gln Leu Phe Gln Glu Tyr Asp Asn His Ile Lys Ser Ser
100         235                 240                 245
102 gtg gtg ggc agt gag cgg aag cga gga atg cag ctg gaa gat ctc aaa      940
103 Val Val Gly Ser Glu Arg Lys Arg Gly Met Gln Leu Glu Asp Leu Lys
104     250                 255                 260
106 cag cag ctc cag cag gcc gag gag gcc ctg gtg gcc aaa cag gag gtg      988
107 Gln Gln Leu Gln Gln Ala Glu Glu Ala Leu Val Ala Lys Gln Glu Val
108 265                 270                 275                 280
110 atc gat aag ctg aag gag gag gcc gag cag cac aag att gtg atg gag     1036
111 Ile Asp Lys Leu Lys Glu Glu Ala Glu Gln His Lys Ile Val Met Glu
112                 285                 290                 295
114 acc gtt ccg gtg ctg aag gcc cag gcg gat atc tac aag gcg gac ttc     1084
115 Thr Val Pro Val Leu Lys Ala Gln Ala Asp Ile Tyr Lys Ala Asp Phe
116             300                 305                 310
118 cag gct gag agg cag gcc cgg gag aag ctg gcc gag aag aag gag ctc     1132
119 Gln Ala Glu Arg Gln Ala Arg Glu Lys Leu Ala Glu Lys Lys Glu Leu
120         315                 320                 325
122 ctg cag gag cag ctg gag cag ctg cag agg gag tac agc aaa ctg aag     1180
123 Leu Gln Glu Gln Leu Glu Gln Leu Gln Arg Glu Tyr Ser Lys Leu Lys
124     330                 335                 340
126 gcc agc tgt cag gag tcg gcc agg atc gag gac atg agg aag cgg cat     1228
127 Ala Ser Cys Gln Glu Ser Ala Arg Ile Glu Asp Met Arg Lys Arg His
128 345                 350                 355                 360
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132                 365                 370                 375
134 tct ccc ctg gcc ctg ccc agc cag agg agg agc ccc ccc gag gag cca     1324
135 Ser Pro Leu Ala Leu Pro Ser Gln Arg Arg Ser Pro Pro Glu Glu Pro
136             380                 385                 390
138 cct gac ttc tgc tgt ccc aag tgc cag tat cag gcc cct gat atg gac     1372
139 Pro Asp Phe Cys Cys Pro Lys Cys Gln Tyr Gln Ala Pro Asp Met Asp
140         395                 400                 405
142 acc ctg cag ata cat gtc atg gag tgc att gag tagggccggc cagtgcaagg   1425
143 Thr Leu Gln Ile His Val Met Glu Cys Ile Glu
144     410                 415
146 ccactgcctg cccgaggacg tgcccgggac cgtgcagtct gcgctttcct ctcccgcctg   1485
148 cctagcccag gatgaagggc tgggtggcca caactgggat gccacctgga gccccaccca   1545
150 ggagctggcc gcggcacctt acgcttcagc tgttgatccg ctggtcccct cttttggggt   1605
152 agatgcggcc ccgatcaggc ctgactcgct gctcttttg ttcccttctg tctgctcgaa   1665
154 ccacttgcct cgggctaatc cctccctctt cctccacccg gcactgggga agtcaagaat   1725
156 ggggcctggg gctctcaggg agaactgctt cccctggcag agctgggtgg cagctcttcc   1785
158 tcccaccgga caccgacccg cccgccgctg tgccctggga gtgctgccct cttaccatgc   1845
160 acacgggtgc tctccttttg ggctgcatgc tattccattt tgcagccaga ccgatgtgta   1905
162 tttaaccagt cactattgat ggacatttgg gttgtttccc atctttttgt taccataaat   1965
164 aatggcatag taaaaaaaaa aaaaaaaaa                                     1994
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168 <211> LENGTH: 419
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178 Ser Gly Gly Pro Ala Ala Asp Gln Asp Val Leu Gly Glu Glu Ser Pro
179             20                  25                  30
182 Leu Gly Lys Pro Ala Met Leu His Leu Pro Ser Glu Gln Gly Ala Pro
183         35                  40                  45
186 Glu Thr Leu Gln Arg Cys Leu Glu Glu Asn Gln Glu Leu Arg Asp Ala
187     50                  55                  60
190 Ile Arg Gln Ser Asn Gln Ile Leu Arg Glu Arg Cys Glu Glu Leu Leu
191 65                  70                  75                  80
194 His Phe Gln Ala Ser Gln Arg Glu Glu Lys Glu Phe Leu Met Cys Lys
195                 85                  90                  95
198 Phe Gln Glu Ala Arg Lys Leu Val Glu Arg Leu Gly Leu Glu Lys Leu
199             100                 105                 110
202 Asp Leu Lys Arg Gln Lys Glu Gln Ala Leu Arg Glu Val Glu His Leu
203         115                 120                 125
206 Lys Arg Cys Gln Gln Gln Met Ala Glu Asp Lys Ala Ser Val Lys Ala
207     130                 135                 140
210 Gln Val Thr Ser Leu Leu Gly Glu Leu Gln Glu Ser Gln Ser Arg Leu
211 145                 150                 155                 160
214 Glu Ala Ala Thr Lys Glu Cys Gln Ala Leu Glu Gly Arg Ala Arg Ala
215                 165                 170                 175
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218 Ala Ser Glu Gln Ala Arg Gln Leu Glu Ser Glu Arg Glu Ala Leu Gln
219             180                 185                 190
222 Gln Gln His Ser Val Gln Val Asp Gln Leu Arg Met Gln Gly Gln Ser
223         195                 200                 205
226 Val Glu Ala Ala Leu Arg Met Glu Arg Gln Ala Ala Ser Glu Glu Lys
227     210                 215                 220
230 Arg Lys Leu Ala Gln Leu Gln Val Ala Tyr His Gln Leu Phe Gln Glu
231 225                 230                 235                 240
234 Tyr Asp Asn His Ile Lys Ser Ser Val Val Gly Ser Glu Arg Lys Arg
235                 245                 250                 255
238 Gly Met Gln Leu Glu Asp Leu Lys Gln Gln Leu Gln Gln Ala Glu Glu
239             260                 265                 270
242 Ala Leu Val Ala Lys Gln Glu Val Ile Asp Lys Leu Lys Glu Glu Ala
243         275                 280                 285
246 Glu Gln His Lys Ile Val Met Glu Thr Val Pro Val Leu Lys Ala Gln
247     290                 295                 300
250 Ala Asp Ile Tyr Lys Ala Asp Phe Gln Ala Glu Arg Gln Ala Arg Glu
251 305                 310                 315                 320
254 Lys Leu Ala Glu Lys Lys Glu Leu Leu Gln Glu Gln Leu Glu Gln Leu
255                 325                 330                 335
258 Gln Arg Glu Tyr Ser Lys Leu Lys Ala Ser Cys Gln Glu Ser Ala Arg
259             340                 345                 350
262 Ile Glu Asp Met Arg Lys Arg His Val Glu Val Ser Gln Ala Pro Leu
263         355                 360                 365
266 Pro Pro Ala Pro Ala Tyr Leu Ser Ser Pro Leu Ala Leu Pro Ser Gln
267     370                 375                 380
270 Arg Arg Ser Pro Pro Glu Glu Pro Pro Asp Phe Cys Cys Pro Lys Cys
271 385                 390                 395                 400
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275                 405                 410                 415
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282 <210> SEQ ID NO: 3
283 <211> LENGTH: 5371
284 <212> TYPE: DNA
285 <213> ORGANISM: Homo sapiens
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288 <221> NAME/KEY: CDS
289 <222> LOCATION: (392)..(3262)
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300 atcatctttc cattgtcttc atggaaaatt gataaatatt tgtgccttcc aactctcgtc    240
302 ttggttgaat gacttcatct taatacaaca tggacaccac gttgctgaaa acatgctttg    300
304 ggactgccac tgaatttatc ttttgcggtt ttatgacaaa gttattagta gtttcccttt    360
306 tttgaattag tattttgaag ttaatatcac a atg agt tca ggc tta tgg agc       412
307                                   Met Ser Ser Gly Leu Trp Ser
308                                   1               5
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310 caa gaa aaa gtc act tca ccc tac tgg gaa gag cgg att ttt tac ttg      460
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312         10                  15                  20
314 ctt ctt caa gaa tgc agc gtt aca gac aaa caa aca caa aag ctc ctt      508
315 Leu Leu Gln Glu Cys Ser Val Thr Asp Lys Gln Thr Gln Lys Leu Leu
316     25                  30                  35
318 aaa gta ccg aag gga agt ata gga cag tat att caa gat cgt tct gtg      556
319 Lys Val Pro Lys Gly Ser Ile Gly Gln Tyr Ile Gln Asp Arg Ser Val
320 40                  45                  50                  55
322 ggg cat tca agg att cct tct gca aaa ggc aag aaa aat cag att gga      604
323 Gly His Ser Arg Ile Pro Ser Ala Lys Gly Lys Lys Asn Gln Ile Gly
324                 60                  65                  70
326 tta aaa att cta gag caa cct cat gca gtt ctc ttt gtt gat gaa aag      652
327 Leu Lys Ile Leu Glu Gln Pro His Ala Val Leu Phe Val Asp Glu Lys
328             75                  80                  85
330 gat gtt gta gag ata aat gaa aag ttc aca gag tta ctt ttg gca att      700
331 Asp Val Val Glu Ile Asn Glu Lys Phe Thr Glu Leu Leu Leu Ala Ile
332         90                  95                  100
334 acc aat tgt gag gag agg ttc agc ctg ttt aaa aac aga aac aga cta      748
335 Thr Asn Cys Glu Glu Arg Phe Ser Leu Phe Lys Asn Arg Asn Arg Leu
336     105                 110                 115
338 agt aaa ggc ctc caa ata gac gtg ggc tgt cct gtg aaa gta cag ctg      796
339 Ser Lys Gly Leu Gln Ile Asp Val Gly Cys Pro Val Lys Val Gln Leu
340 120                 125                 130                 135
342 aga tct ggg gaa gaa aaa ttt cct gga gtt gta cgc ttc aga gga ccc      844
343 Arg Ser Gly Glu Glu Lys Phe Pro Gly Val Val Arg Phe Arg Gly Pro
344                 140                 145                 150
346 ctg tta gca gag agg aca gtc tcc gga ata ttc ttt gga gtt gaa ttg      892
347 Leu Leu Ala Glu Arg Thr Val Ser Gly Ile Phe Phe Gly Val Glu Leu
348             155                 160                 165
350 ctg gaa gaa ggt cgt ggt caa ggt ttc act gac ggg gtg tac caa ggg      940
351 Leu Glu Glu Gly Arg Gly Gln Gly Phe Thr Asp Gly Val Tyr Gln Gly
352         170                 175                 180
354 aaa cag ctt ttt cag tgt gat gaa gat tgt ggc gtg ttt gtt gca ttg      988
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356     185                 190                 195
358 gac aag cta gaa ctc ata gaa gat gat gac act gca ttg gaa agt gat     1036
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360 200                 205                 210                 215
362 tac gca ggt cct ggg gac aca atg cag gtc gaa ctt cct cct ttg gaa     1084
363 Tyr Ala Gly Pro Gly Asp Thr Met Gln Val Glu Leu Pro Pro Leu Glu
364                 220                 225                 230
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367 Ile Asn Ser Arg Val Ser Leu Lys Val Gly Glu Thr Ile Glu Ser Gly
368             235                 240                 245
370 aca gtt ata ttc tgt gat gtt ttg cca gga aaa gaa agc tta gga tat     1180
371 Thr Val Ile Phe Cys Asp Val Leu Pro Gly Lys Glu Ser Leu Gly Tyr
372         250                 255                 260
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L:12 M:270 C: Current Application Number differs, Replaced Current Application Number